

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/133,119DATE: 05/18/1999  
TIME: 15:36:25

INPUT SET: S31902.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

 #7

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Le, Junming  
Vilcek, Jan  
Daddona, Peter E.  
Ghrayeb, John  
Knight, David M.  
Siegel, Scott A.

ENTERED

(ii) TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES  
OF HUMAN TUMOR NECROSIS FACTOR

(iii) NUMBER OF SEQUENCES: 19

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
(B) STREET: Two Militia Drive  
(C) CITY: Lexington  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02173

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/133,119  
(B) FILING DATE:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/570,674  
(B) FILING DATE: 11-DEC-1995

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/324,799  
(B) FILING DATE: 18-OCT-1994

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/192,093  
(B) FILING DATE: 04-FEB-1994

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47 (vii) PRIOR APPLICATION DATA:  
48 (A) APPLICATION NUMBER: 08/192,102  
49 (B) FILING DATE: 04-FEB-1994  
50  
51 (vii) PRIOR APPLICATION DATA:  
52 (A) APPLICATION NUMBER: 08/192,861  
53 (B) FILING DATE: 04-FEB-1994  
54  
55 (vii) PRIOR APPLICATION DATA:  
56 (A) APPLICATION NUMBER: US 08/013,413  
57 (B) FILING DATE: 02-FEB-1993  
58  
59 (vii) PRIOR APPLICATION DATA:  
60 (A) APPLICATION NUMBER: US 08/010,406  
61 (B) FILING DATE: 29-JAN-1993  
62  
63 (vii) PRIOR APPLICATION DATA:  
64 (A) APPLICATION NUMBER: US 07/943,852  
65 (B) FILING DATE: 11-SEP-1992  
66  
67  
68  
69 (vii) PRIOR APPLICATION DATA:  
70 (A) APPLICATION NUMBER: US 07/853,606  
71 (B) FILING DATE: 18-MAR-1992  
72  
73 (vii) PRIOR APPLICATION DATA:  
74 (A) APPLICATION NUMBER: US 07/670,827  
75 (B) FILING DATE: 18-MAR-1991  
76  
77 (viii) ATTORNEY/AGENT INFORMATION:  
78 (A) NAME: Brook, David E.  
79 (B) REGISTRATION NUMBER: 22,592  
80 (C) REFERENCE/DOCKET NUMBER: NYU93-01M4A  
81  
82 (ix) TELECOMMUNICATION INFORMATION:  
83 (A) TELEPHONE: (617) 861-6240  
84 (B) TELEFAX: (617) 861-9540  
85  
86  
87 (2) INFORMATION FOR SEQ ID NO:1:  
88  
89 (i) SEQUENCE CHARACTERISTICS:  
90 (A) LENGTH: 157 amino acids  
91 (B) TYPE: amino acid  
92 (D) TOPOLOGY: linear  
93  
94 (ii) MOLECULE TYPE: peptide  
95  
96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
97  
98 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val  
99 1 5 10 15

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100
101 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
102                20                      25                      30
103
104 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
105                35                      40                      45
106
107 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
108                50                      55                      60
109
110 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
111        65                      70                      75                      80
112
113 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
114                85                      90                      95
115
116 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
117                100                      105                      110
118
119 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
120                115                      120                      125
121
122 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
123        130                      135                      140
124
125 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
126        145                      150                      155
127
128
129

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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149 GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA 48
150 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
151    1                      5                      10                      15
152

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153  GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC 96
154  Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
155           20           25           30
156
157  ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA 144
158  Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
159           35           40           45
160
161  AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC 192
162  Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
163           50           55           60
164
165  AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT 240
166  Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
167           65           70           75           80
168
169  GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC 288
170  Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
171           85           90           95
172
173  ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA 321
174  Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
175           100           105
176
177
178  (2) INFORMATION FOR SEQ ID NO:3:
179
180      (i) SEQUENCE CHARACTERISTICS:
181          (A) LENGTH: 107 amino acids
182          (B) TYPE: amino acid
183          (D) TOPOLOGY: linear
184
185      (ii) MOLECULE TYPE: protein
186
187      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
188
189  Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
190      1           5           10           15
191
192  Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
193           20           25           30
194
195  Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
196           35           40           45
197
198  Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
199           50           55           60
200
201  Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
202           65           70           75           80
203
204  Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
205           85           90           95

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206
207 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
208          100                      105
209
210 (2) INFORMATION FOR SEQ ID NO:4:
211
212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 357 base pairs
214 (B) TYPE: nucleic acid
215 (C) STRANDEDNESS: single
216 (D) TOPOLOGY: linear
217
218 (ii) MOLECULE TYPE: cDNA
219
220
221 (ix) FEATURE:
222 (A) NAME/KEY: CDS
223 (B) LOCATION: 1..357
224
225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
227
228 GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA 48
229 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
230 1          5          10          15
231
232 TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC 96
233 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
234          20          25          30
235
236 TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT 144
237 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
238          35          40          45
239
240 GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG 192
241 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
242          50          55          60
243
244 TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT 240
245 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
246          65          70          75          80
247
248 GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT 288
249 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
250          85          90          95
251
25

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**SEQUENCE VERIFICATION REPORT**  
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Original Text